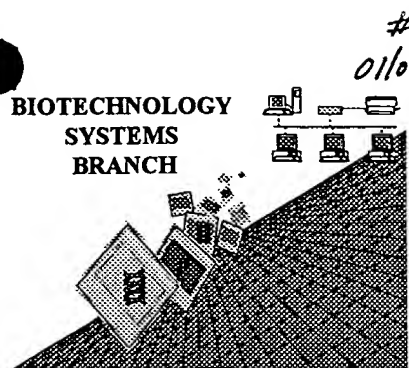


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/291,931

Art Unit / Team No. : 01/16

Date Processed by STIC: 4/28/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/29/93/

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
All text must be visible on page.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) features section that some may be missing.
- 7 Wrong Designation Sequence(s) contain amino acid or nucleic acid designators which are not standard
representations as per the Sequence Rules (Please refer to paragraph 1.822)
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (x1) SEQUENCE DESCRIPTION: SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)
(Sec. 1.823 of new Sequence Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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RAW SEQUENCE LISTING

PATENT APPLICATION US/09/291,931

 DATE: 04/28/1999
 TIME: 11:16:09

Input Set: I291931.RAW

This Raw Listing contains the General Information
 Section and up to first 5 pages.

Does Not Comply
 Corrected Diskette Needed

BP 1,3

1 <110> APPLICANT: Kretz, Keith
 2 <120> TITLE OF INVENTION: Novel Phytase
 3 <130> FILE REFERENCE: 09010/029003
 4 <140> CURRENT APPLICATION NUMBER: US/09/291,931
 5 <141> CURRENT FILING DATE: 1999-04-13
 6 <150> EARLIER APPLICATION NUMBER: 09/259,214
 7 <151> EARLIER FILING DATE: 1999-03-01
 8 <150> EARLIER APPLICATION NUMBER: 08/910,798
 9 <151> EARLIER FILING DATE: 1997-08-13
 10 <160> NUMBER OF SEQ ID NOS: 4
 11 <170> SOFTWARE: PatentIn Ver. 2.0
 12 <210> SEQ ID NO 1
 13 <211> LENGTH: 1323
 14 <212> TYPE: DNA
 15 <213> ORGANISM: Escherichia coli
 16 <220> FEATURE:
 17 <221> NAME/KEY: CDS
 18 <222> LOCATION: (1)..(1323)
 19 <400> SEQUENCE: 1
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 22 1 5 10 15
 23 ccg caa tct gca ttc gct cag agt gag ccg gag ctg aag ctg gaa agt 96
 24 Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser
 25 20 25 30
 26 gtg gtg att gtc agt cgt cat ggt gtg cgt gct cca acc aag gcc acg 144
 27 Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr
 28 35 40 45
 29 caa ctg atg cag gat gtc acc cca gac gca tgg cca acc tgg ccg gta 192
 30 Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val
 31 50 55 60
 32 *all* *10* *Even* *100* *110* *120* *125* *130* *135* *140* *145* *150* *155* *160* *165* *170* *175* *180* *185* *190* *195* *200* *205* *210* *215* *220* *225* *230* *235* *240* *245* *250* *255* *260* *265* *270* *275* *280* *285* *290* *295* *300* *305* *310* *315* *320* *325* *330* *335* *340* *345* *350* *355* *360* *365* *370* *375* *380* *385* *390* *395* *400* *405* *410* *415* *420* *425* *430* *435* *440* *445* *450* *455* *460* *465* *470* *475* *480* *485* *490* *495* *500* *505* *510* *515* *520* *525* *530* *535* *540* *545* *550* *555* *560* *565* *570* *575* *580* *585* *590* *595* *600* *605* *610* *615* *620* *625* *630* *635* *640* *645* *650* *655* *660* *665* *670* *675* *680* *685* *690* *695* *700* *705* *710* *715* *720* *725* *730* *735* *740* *745* *750* *755* *760* *765* *770* *775* *780* *785* *790* *795* *800* *805* *810* *815* *820* *825* *830* *835* *840* *845* *850* *855* *860* *865* *870* *875* *880* *885* *890* *895* *900* *905* *910* *915* *920* *925* *930* *935* *940* *945* *950* *955* *960* *965* *970* *975* *980* *985* *990* *995* *1000* *1005* *1010* *1015* *1020* *1025* *1030* *1035* *1040* *1045* *1050* *1055* *1060* *1065* *1070* *1075* *1080* *1085* *1090* *1095* *1100* *1105* *1110* *1115* *1120* *1125* *1130* *1135* *1140* *1145* *1150* *1155* *1160* *1165* *1170* *1175* *1180* *1185* *1190* *1195* *1200* *1205* *1210* *1215* *1220* *1225* *1230* *1235* *1240* *1245* *1250* *1255* *1260* *1265* *1270* *1275* *1280* *1285* *1290* *1295* *1300* *1305* *1310* *1315* *1320* *1323*
 32 aaa ctg ggt tgg ctg aca ccg cga ggt ggt gag cta atc gcc tat ctc 240
 33 Lys Leu Gly Trp Leu Thr Pro Xaa Gly Gly Glu Leu Ile Ala Tyr Leu
 34 65 70 75 80
 35 gga cat tac caa cgc cag cgt ctg gta gcc gac gga ttg ctg gcg aaa 288
 36 Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys
 37 85 90 95
 38 aaag ggc tgc ccg cag tct ggt cag gtc gcg att att gct gat gtc gac 336
 39 Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp
 40 100 105 110
 41 gag cgt acc cgt aaa aca ggc gaa gcc ttc gcc gcc ggg ctg gca cct 384
 42 Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro
 43 115 120 125
 44 gac tgt gca ata acc gta cat acc cag gca gat acg tcc agt ccc gat 432

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RAW SEQUENCE LISTING
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45	Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp	
46	130 135 140	
47	ccg tta ttt aat cct cta aaa act ggc gtt tgc caa ctg gat aac gcg	480
48	Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala	
49	145 150 155 160	
50	aac gtg act gac gcg atc ctc agc agg gca gga ggg tca att gct gac	528
51	Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp	
52	165 170 175	
53	ttt acc ggg cat cgg caa acg gcg ttt cgc gaa ctg gaa cgg gtg ctt	576
54	Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu	
55	180 185 190	
56	aat ttt ccg caa tca aac ttg tgc ctt aaa cgt gag aaa cag gac gaa	624
57	Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu	
58	195 200 205	
59	agc tgt tca tta acg cag gca tta cca tcg gaa ctc aag gtg agc gcc	672
60	Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala	
61	210 215 220	
62	gac aat gtc tca tta acc ggt gcg gta agc ctc gca tca atg ctg acg	720
63	Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr	
64	225 230 235 240	
65	gag ata ttt ctc ctg caa caa gca cag gga atg ccg gag ccg ggg tgg	768
66	Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp	
67	245 250 255	
68	gga agg atc acc gat tca cac cag tgg aac acc ttg cta agt ttg cat	816
69	Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His	
70	260 265 270	
71	aac gcg caa ttt tat ttg cta caa cgc acg cca gag gtt gcc cgc agc	864
72	Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser	
73	275 280 285	
74	cgc gcc acc ccg tta ttg gat ttg atc atg gca gcg ttg acg ccc cat	912
75	Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His	
76	290 295 300	
77	cca ccg caa aaa cag gcg tat ggt gtg aca tta ccc act tca gta ctg	960
78	Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu	
79	305 310 315 320	
80	ttt att gcc gga cac gat act aat ctg gca aat ctc ggc ggc gca ctg	1008
81	Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu	
82	325 330 335	
83	gag ctc aac tgg acg ctt ccc ggt cag ccg gat aac acg ccg cca ggt	1056
84	Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly	
85	340 345 350	
86	ggt gaa ctg gtg ttt gaa cgc tgg cgt ccg cta agc gat aac agc cag	1104
87	Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln	
88	355 360 365	
89	tgg att cag gtt tcg ctg gtc ttc cag act tta cag cag atg cgt gat	1152
90	Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp	
91	370 375 380	
92	aaa acg ccg ctg tca tta aat acg ccg ccc gga gag gtg aaa ctg acc	1200
93	Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr	
94	385 390 395 400	

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RAW SEQUENCE LISTING PATENT APPLICATION US/09/291,931

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95      ctg gca gga tgt gaa gag cga aat gcg cag ggc atg tgt tcg ttg gca      1248
96      Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala
97                      405                      410                      415
98      ggt ttt acg caa atc gtg aat gaa gca cgc ata ccg gcg tgc agt ttg      1296
99      Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu
100                      420                      425                      430
101      aga tct cat cac cat cac cat cac taa      1323
102      Arg Ser His His His His His His
103                      435                      440
104      <210> SEQ ID NO 2
105      <211> LENGTH: 440
106      <212> TYPE: PRT
107      <213> ORGANISM: Escherichia coli
108      <400> SEQUENCE: 2
109      Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr
110           1           5           10           15
111      Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser
112           20           25           30
113      Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr
114           35           40           45
115      Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val
116           50           55           60
117      Lys Leu Gly Trp Leu Thr Pro Xaa Gly Gly Glu Leu Ile Ala Tyr Leu
118           65           70           75           80
119      Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys
120           85           90           95
121      Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp
122           100          105          110
123      Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro
124           115          120          125
125      Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp
126           130          135          140
127      Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala
128           145          150          155          160
129      Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp
130           165          170          175
131      Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu
132           180          185          190
133      Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu
134           195          200          205
135      Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala
136           210          215          220
137      Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr
138           225          230          235          240
139      Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp
140           245          250          255
141      Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His
142           260          265          270
143      Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser
144           275          280          285

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W-->

see
Jan 10

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RAW SEQUENCE LISTING PATENT APPLICATION US/09/291,931

DATE: 04/28/1999
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Input Set: I291931.RAW

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145      Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His
146          290                      295                      300
147      Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu
148          305                      310                      315                      320
149      Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu
150                      325                      330                      335
151      Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly
152                      340                      345                      350
153      Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln
154          355                      360                      365
155      Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp
156          370                      375                      380
157      Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr
158          385                      390                      395                      400
159      Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala
160                      405                      410                      415
161      Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu
162                      420                      425                      430
163      Arg Ser His His His His His His
164          435                      440

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165 <210> SEQ ID NO 3

166 <211> LENGTH: 49

167 <212> TYPE: DNA

168 <213> ORGANISM: Artificial Sequence

169 <220> FEATURE:

170 <223> OTHER INFORMATION: Description of Artificial Sequence:

171 oligonucleotide

172 <400> SEQUENCE: 3

173 gtttctgaat tcaaggagga attttaaata aagcgatctt aatcccatt

49

174 <210> SEQ ID NO 4

175 <211> LENGTH: 33

176 <212> TYPE: DNA

177 <213> ORGANISM: Artificial Sequence

178 <220> FEATURE:

179 <223> OTHER INFORMATION: Description of Artificial Sequence:

180 oligonucleotide

181 <400> SEQUENCE: 4

182 gtttctggat ccttacaaac tgcacgccg tat

33

Input Set: I291931.RAW

Line	? Error/Warning	Original Text
32	W "N" or "Xaa" used: Feature required	aaa ctg ggt tgg ctg aca ccg cgn ggt ggt g
117	W "N" or "Xaa" used: Feature required	Lys Leu Gly Trp Leu Thr Pro Xaa Gly Gly G